

05/30
10/11HG

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/779,050A

DATE: 06/14/2001
TIME: 13:03:05

Input Set : A:\A-570B.ST25.txt
Output Set: N:\CRF3\06142001\I779050A.raw

3 <110> APPLICANT: BOYLE, WILLIAM
 4 HSU, HAILING
 6 <120> TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
 8 <130> FILE REFERENCE: A-570B
 10 <140> CURRENT APPLICATION NUMBER: 09/779,050A
 11 <141> CURRENT FILING DATE: 2001-02-12
 13 <150> PRIOR APPLICATION NUMBER: 60/181,800
 14 <151> PRIOR FILING DATE: 2000-02-11
 16 <160> NUMBER OF SEQ ID NOS: 52
 18 <170> SOFTWARE: PatentIn version 3.0
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 1173
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Homo sapiens
 25 <220> FEATURE:
 26 <221> NAME/KEY: CDS
 27 <222> LOCATION: (143)..(997)
 29 <400> SEQUENCE: 1
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 32 acaaacacag ataacagggaa atgatccatt ccctgtggtc acttattcta aaggccccaa 120
 34 ccttcaagt tcaagtagtg at 'atg gat gac tcc aca gaa agg gag cag tca 172
 35 Met Asp Asp Ser Thr Glu Arg Glu Gln Ser
 36 1 5 10
 38 cgc ctt act tct tgc ctt aag aaa aga gaa gaa atg aaa ctg aag gag 220
 39 Arg Leu Thr Ser Cys Leu Lys Lys Arg Glu Glu Met Lys Leu Lys Glu
 40 15 20 25
 42 tgt gtt tcc atc ctc cca cgg aag gaa agc ccc tct gtc cga tcc tcc 268
 43 Cys Val Ser Ile Leu Pro Arg Lys Glu Ser Pro Ser Val Arg Ser Ser
 44 30 35 40
 46 aaa gac gga aag ctg ctg gct gca acc ttg ctg ctg gca ctg ctg tct 316
 47 Lys Asp Gly Lys Leu Leu Ala Ala Thr Leu Leu Ala Leu Leu Ser
 48 45 50 55
 50 tgc tgc ctc acg gtg gtg tct ttc tac cag gtg gcc gcc ctg caa ggg 364
 51 Cys Cys Leu Thr Val Val Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly
 52 60 65 70
 54 gac ctg gcc agc ctc cgg gca gag ctg cag ggc cac cac gcg gag aag 412
 55 Asp Leu Ala Ser Leu Arg Ala Glu Leu Gln Gly His His Ala Glu Lys
 56 75 80 85 90
 58 ctg cca gca gga gca gga gcc ccc aag gcc ggc ctg gag gaa gct cca 460
 59 Leu Pro Ala Gly Ala Gly Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro
 60 95 100 105
 62 gct gtc acc gcg gga ctg aaa atc ttt gaa cca cca gct cca gga gaa 508
 63 Ala Val Thr Ala Gly Leu Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu
 64 110 115 120
 66 ggc aac tcc agt cag aac agc aga aat aag cgt gcc gtt cag ggt cca 556
 67 Gly Asn Ser Ser Gln Asn Ser Arg Asn Lys Arg Ala Val Gln Gly Pro
 68 125 130 135

ENTERED
See p.5

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70	gaa	gaa	aca	gtc	act	caa	gac	tgc	ttg	caa	ctg	att	gca	gac	agt	gaa		604
71	Glu	Glu	Thr	Val	Thr	Gln	Asp	Cys	Leu	Gln	Leu	Ile	Ala	Asp	Ser	Glu		
72	140					145					150							
74	aca	cca	act	ata	caa	aaa	gga	tct	tac	aca	ttt	gtt	cca	tgg	ctt	ctc		652
75	Thr	Pro	Thr	Ile	Gln	Lys	Gly	Ser	Tyr	Thr	Phe	Val	Pro	Trp	Leu	Leu		
76	155					160					165					170		
78	agc	ttt	aaa	agg	gga	agt	gcc	cta	gaa	gaa	aaa	gag	aat	aaa	ata	ttg		700
79	Ser	Phe	Lys	Arg	Gly	Ser	Ala	Leu	Glu	Glu	Lys	Glu	Asn	Lys	Ile	Leu		
80						175				180					185			
82	gtc	aaa	gaa	act	ggt	tac	ttt	ttt	ata	tat	gtt	cag	gtt	tta	tat	act		748
83	Val	Lys	Glu	Thr	Gly	Tyr	Phe	Phe	Ile	Tyr	Gly	Gln	Val	Leu	Tyr	Thr		
84						190				195					200			
86	gat	aag	acc	tac	gcc	atg	gga	cat	cta	att	cag	agg	aag	gtc	cat			796
87	Asp	Lys	Thr	Tyr	Ala	Met	Gly	His	Leu	Ile	Gln	Arg	Lys	Lys	Val	His		
88						205				210					215			
90	gtc	ttt	ggg	gat	gaa	ttg	agt	ctg	gtg	act	ttg	ttt	cga	tgt	att	caa		844
91	Val	Phe	Gly	Asp	Glu	Leu	Ser	Leu	Val	Thr	Leu	Phe	Arg	Cys	Ile	Gln		
92						220				225					230			
94	aat	atg	cct	gaa	aca	cta	ccc	aat	aat	tcc	tgc	tat	tca	gct	ggc	att		892
95	Asn	Met	Pro	Glu	Thr	Leu	Pro	Asn	Asn	Ser	Cys	Tyr	Ser	Ala	Gly	Ile		
96						235				240			245		250			
98	gca	aaa	ctg	gaa	gaa	gga	gat	gaa	ctc	caa	ttt	gca	ata	cca	aga	gaa		940
99	Ala	Lys	Leu	Glu	Glu	Gly	Asp	Glu	Leu	Gln	Leu	Ala	Ile	Pro	Arg	Glu		
100						255				260					265			
102	aat	gca	caa	ata	tca	ctg	gat	gga	gat	gtc	aca	ttt	ttt	ggt	gca	ttg		988
103	Asn	Ala	Gln	Ile	Ser	Leu	Asp	Gly	Asp	Val	Thr	Phe	Phe	Gly	Ala	Leu		
104						270				275					280			
106	aaa	ctg	ctg	tgacacctactt	acaccatgtc	tgttagctatt	ttcctccctt										1037	
107	Lys	Leu	Leu															
108			285															
110	tctctgtacc	tctaagaaga	aagaatctaa	ctgaaaatac	aaaaaaaaaaaa	aaaaaaaaaaaa	aaaaaaaaaaaa										1097	
112	aaaaaaaaagt	agtaaaaaaaaa	aaaaaaaaaaa	aaaaaaaaaaa	aaaaaaaaaaa	aaaaaaaaaaa	aaaaaaaaaaa										1157	
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118	<211>	LENGTH:	285															
119	<212>	TYPE:	PRT															
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128	Lys	Lys	Arg	Glu	Glu	Met	Lys	Leu	Lys	Glu	Cys	Val	Ser	Ile	Leu	Pro		
129						20				25					30			
132	Arg	Lys	Glu	Ser	Pro	Ser	Val	Arg	Ser	Ser	Lys	Asp	Gly	Lys	Leu	Leu		
133						35			40						45			
136	Ala	Ala	Thr	Leu	Leu	Leu	Ala	Leu	Leu	Ser	Cys	Cys	Leu	Thr	Val	Val		
137						50			55						60			
140	Ser	Phe	Tyr	Gln	Val	Ala	Ala	Leu	Gln	Gly	Asp	Leu	Ala	Ser	Leu	Arg		
141	65				70					75					80			
144	Ala	Glu	Leu	Gln	Gly	His	His	Ala	Glu	Lys	Leu	Pro	Ala	Gly	Ala	Gly		

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145	85	90	95	
148	Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu			
149	100	105	110	
152	Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn			
153	115	120	125	
156	Ser Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Val Thr Gln			
157	130	135	140	
160	Asp Cys Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys			
161	145	150	155	160
164	Gly Ser Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser			
165	165	170	175	
168	Ala Leu Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr			
169	180	185	190	
172	Phe Phe Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met			
173	195	200	205	
176	Gly His Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu			
177	210	215	220	
180	Ser Leu Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu			
181	225	230	235	240
184	Pro Asn Asn Ser Cys Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly			
185	245	250	255	
188	Asp Glu Leu Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu			
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198	<212> TYPE: DNA			
199	<213> ORGANISM: Mus musculus			
201	<220> FEATURE:			
202	<221> NAME/KEY: CDS			
203	<222> LOCATION: (52)..(978)			
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210	gag tct gca aag acc ctg cca cca ccg tgc ctc tgt ttt tgc tcc gag		105	
211	Glu Ser Ala Lys Thr Leu Pro Pro Pro Cys Leu Cys Phe Cys Ser Glu			
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214	aaa gga gaa gat atg aaa gtg gga tat gat ccc atc act ccg cag aag		153	
215	Lys Gly Glu Asp Met Lys Val Gly Tyr Asp Pro Ile Thr Pro Gln Lys			
216	20	25	30	
218	gag gag ggt gcc tgg ttt ggg atc tgc agg gat gga agg ctg ctg gct		201	
219	Glu Glu Gly Ala Trp Phe Gly Ile Cys Arg Asp Gly Arg Leu Leu Ala			
220	35	40	45	50
222	gct acc ctc ctg ctg gcc ctg ttg tcc agc agt ttc aca gcg atg tcc		249	
223	Ala Thr Leu Leu Ala Leu Leu Ser Ser Ser Phe Thr Ala Met Ser			
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226	ttg tac cag ttg gct gcc caa gca gac ctg atg aac ctg cgc atg		297	

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Input Set : A:\A-570B.ST25.txt
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227	Leu	Tyr	Gln	Leu	Ala	Ala	Leu	Gln	Ala	Asp	Leu	Met	Asn	Leu	Arg	Met	
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230	gag	ctg	cag	agc	tac	cga	ggt	tca	gca	aca	cca	gcc	gcc	gct	ggt	gct	345
231	Glu	Leu	Gln	Ser	Tyr	Arg	Gly	Ser	Ala	Thr	Pro	Ala	Ala	Ala	Gly	Ala	
232				85				90			95						
234	cca	gag	ttg	acc	gct	gga	gtc	aaa	ctc	ctg	aca	ccg	gca	gct	cct	cga	393
235	Pro	Glu	Leu	Thr	Ala	Gly	Val	Lys	Leu	Leu	Thr	Pro	Ala	Ala	Pro	Arg	
236				100				105			110						
238	ccc	cac	aac	tcc	agc	cgc	ggc	cac	agg	aac	aga	cgc	gct	ttc	cag	gga	441
239	Pro	His	Asn	Ser	Ser	Arg	Gly	His	Arg	Asn	Arg	Arg	Ala	Phe	Gln	Gly	
240	115				120				125			130					
242	cca	gag	gaa	aca	gaa	caa	gat	gta	gac	ctc	tca	gct	cct	cct	gca	cca	489
243	Pro	Glu	Glu	Thr	Glu	Gln	Asp	Val	Asp	Leu	Ser	Ala	Pro	Pro	Ala	Pro	
244					135				140			145					
246	tgc	ctg	cct	gga	tgc	cgc	cat	tct	caa	cat	gat	aat	gga	atg	aac		537
247	Cys	Leu	Pro	Gly	Cys	Arg	His	Ser	Gln	His	Asp	Asp	Asn	Gly	Met	Asn	
248					150				155			160					
250	ctc	aga	aac	atc	att	caa	gac	tgt	ctg	cag	ctg	att	gca	gac	agc	gac	585
251	Leu	Arg	Asn	Ile	Ile	Gln	Asp	Cys	Leu	Gln	Leu	Ile	Ala	Asp	Ser	Asp	
252					165				170			175					
254	acg	ccg	act	ata	cga	aaa	gga	act	tac	aca	ttt	gtt	cca	tgg	ctt	ctc	633
255	Thr	Pro	Thr	Ile	Arg	Lys	Gly	Thr	Tyr	Thr	Phe	Val	Pro	Trp	Leu	Leu	
256					180				185			190					
258	agc	ttt	aaa	aga	aat	gcc	ttg	gag	gag	aaa	gag	aac	aaa	ata	gtg		681
259	Ser	Phe	Lys	Arg	Gly	Asn	Ala	Leu	Glu	Glu	Lys	Glu	Asn	Lys	Ile	Val	
260	195				200				205			210					
262	gtg	agg	caa	aca	ggc	tat	ttc	ttc	atc	tac	agc	cag	gtt	cta	tac	acg	729
263	Val	Arg	Gln	Thr	Gly	Tyr	Phe	Phe	Ile	Tyr	Ser	Gln	Val	Leu	Tyr	Thr	
264					215				220			225					
266	gac	ccc	atc	ttt	gct	atg	ggt	cat	gtc	atc	cag	agg	aaa	gta	cac		777
267	Asp	Pro	Ile	Phe	Ala	Met	Gly	His	Val	Ile	Gln	Arg	Lys	Lys	Val	His	
268					230				235			240					
270	gtc	ttt	ggg	gac	gag	ctg	agc	ctg	gtg	acc	ctg	ttc	cga	tgt	att	cag	825
271	Val	Phe	Gly	Asp	Glu	Leu	Ser	Leu	Val	Thr	Leu	Phe	Arg	Cys	Ile	Gln	
272					245				250			255					
274	aat	atg	ccc	aaa	aca	ctg	ccc	aac	aat	tcc	tgc	tac	ttt	ggt	gcc	atc	873
275	Asn	Met	Pro	Lys	Thr	Leu	Pro	Asn	Asn	Ser	Cys	Tyr	Leu	Ala	Gly	Ile	
276					260				265			270					
278	gcg	agg	ctg	gaa	gaa	gga	gat	gag	att	cag	ctt	gca	att	cct	cggt	gag	921
279	Ala	Arg	Leu	Glu	Glu	Gly	Asp	Glu	Ile	Gln	Leu	Ala	Ile	Pro	Arg	Glu	
280	275				280				285			290					
282	aat	gca	cag	att	tca	cgc	aac	gga	gac	gac	acc	ttc	ttt	ggt	gcc	cta	969
283	Asn	Ala	Gln	Ile	Ser	Arg	Asn	Gly	Asp	Asp	Thr	Phe	Phe	Gly	Ala	Leu	
284					295				300			305					
286	aaa	ctg	ctg	'taactcaactt	gctggagtgc	gtgatcccct	tccctcgct										1018
287	Lys	Leu	Leu														
290	tctctgtacc	tccgagggag	aaacagacga	ctggaaaaat	aaaagatggg	gaaagccgtc											1078
292	agcgaaagt	ttctctgtac	ccgttgaatc	tgatccaaac	caggaaatat	aacagacagc											1138
294	c																1139

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297 <210> SEQ ID NO: 4
 298 <211> LENGTH: 309
 299 <212> TYPE: PRT
 300 <213> ORGANISM: Mus musculus
 302 <400> SEQUENCE: 4
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 308 Ser Glu Lys Gly Glu Asp Met Lys Val Gly Tyr Asp Pro Ile Thr Pro
 309 20 25 30
 312 Gln Lys Glu Glu Gly Ala Trp Phe Gly Ile Cys Arg Asp Gly Arg Leu
 313 35 40 45
 316 Leu Ala Ala Thr Leu Leu Ala Leu Leu Ser Ser Ser Phe Thr Ala
 317 50 55 60
 320 Met Ser Leu Tyr Gln Leu Ala Ala Leu Gln Ala Asp Leu Met Asn Leu
 321 65 70 75 80
 324 Arg Met Glu Leu Gln Ser Tyr Arg Gly Ser Ala Thr Pro Ala Ala
 325 85 90 95
 328 Gly Ala Pro Glu Leu Thr Ala Gly Val Lys Leu Leu Thr Pro Ala Ala
 329 100 105 110
 332 Pro Arg Pro His Asn Ser Ser Arg Gly His Arg Asn Arg Arg Ala Phe
 333 115 120 125
 336 Gln Gly Pro Glu Glu Thr Glu Gln Asp Val Asp Leu Ser Ala Pro Pro
 337 130 135 140
 340 Ala Pro Cys Leu Pro Gly Cys Arg His Ser Gln His Asp Asp Asn Gly
 341 145 150 155 160
 344 Met Asn Leu Arg Asn Ile Ile Gln Asp Cys Leu Gln Leu Ile Ala Asp
 345 165 170 175
 348 Ser Asp Thr Pro Thr Ile Arg Lys Gly Thr Tyr Thr Phe Val Pro Trp
 349 180 185 190
 352 Leu Leu Ser Phe Lys Arg Gly Asn Ala Leu Glu Glu Lys Glu Asn Lys
 353 195 200 205
 356 Ile Val Val Arg Gln Thr Gly Tyr Phe Phe Ile Tyr Ser Gln Val Leu
 357 210 215 220
 360 Tyr Thr Asp Pro Ile Phe Ala Met Gly His Val Ile Gln Arg Lys Lys
 361 225 230 235 240
 364 Val His Val Phe Gly Asp Glu Leu Ser Leu Val Thr Leu Phe Arg Cys
 365 245 250 255
 368 Ile Gln Asn Met Pro Lys Thr Leu Pro Asn Asn Ser Cys Tyr Leu Ala
 369 260 265 270
 372 Gly Ile Ala Arg Leu Glu Glu Gly Asp Glu Ile Gln Leu Ala Ile Pro
 373 275 280 285
 376 Arg Glu Asn Ala Gln Ile Ser Arg Asn Gly Asp Asp Thr Phe Phe Gly
 377 290 295 300
 380 Ala Leu Lys Leu Leu
 381 305
 384 <210> SEQ ID NO: 5
 385 <211> LENGTH: 278
 386 <212> TYPE: PRT
 387 <213> ORGANISM: Homo sapiens

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/779,050A

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Input Set : A:\A-570B.ST25.txt
Output Set: N:\CRF3\06142001\I779050A.raw

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L:401 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
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L:407 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
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L:468 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:471 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:474 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:477 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:480 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
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L:1159 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1162 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1168 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:26
L:1181 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
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L:1218 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:1221 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:1224 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
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